SEQUENCE LISTING

<110> Yayon, Avner
Rom, Eran
Thomassen-Wolf, Elisabeth
Borges, Eric

<120> ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE ACTIVATION, METHODS OF SCREENING AND USES THEREOF

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<140> US 10/734,661
<141> 2003-12-15

<150> US 60/299,187
<151> 2001-06-20

<150> PCT/IL02/00494
<151> 2002-06-20

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<302> Fully synthetic human combinatorial antibody libraries (HuCAL) based on modular consensus frameworks and CDRs randomized with trinucleotides.
<303> J Mol Biol
<304> 296
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<306> 57-86
<307> 2000-02-11
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<300>
<301> knappik et al
<302> Fully synthetic human combinatorial antibody libraries (HuCAL) based on modular consensus frameworks and CDRs randomized with trinucleotides.
<303> j mol biol
<304> 296
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cgtatgttgt gtggaattgt gagcggataa caatttcaca caggaaacag ctatgaccat 4140

gattacgaat t 4151

<210> 54
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<220>
<221> misc_feature
<222> (253)..(255)
<223> NNN=ACT OR GTT

<400> 54
gatatccaga tgacccagag cccgtctagc ctgagcgcga gcgtgggtga tcgtgtgacc 60

attacctgca gagcgagcca gggcattagc agctatctgg cgtggtacca gcagaaacca 120

ggtaaagcac cgaaactatt aatttatgca gccagcagct tgcaaagcgg ggtcccgtcc 180

cgttttagcg gctctggatc cggcactgat tttaccctga ccattagcag cctgcaacct 240

gaagactttg cgnnntatta ttgccagacc tttggccagg gtacgaaagt tgaaattaaa 300

cgtacg 306

<210> 55
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 55
gatatccaga tgacccagag cccgtctagc ctgagcgcga gcgtgggtga tcgtgtgacc 60

attacctgca gagcgagcca gggcattagc agctatctgg cgtggtacca gcagaaacca 120

ggtaaagcac cgaaactatt aatttatgca gccagcagct tgcaaagcgg ggtcccgtcc 180

cgttttagcg gctctggatc cggcactgat tttaccctga ccattagcag cctgcaacct 240

gaagactttg cggtttatta ttgctttcag tatggttcta ttcctcctac ctttggccag 300

ggtacgaaag ttgaaattaa acgtacg 327

<210> 56
<211> 309
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<220>
<221> misc_feature
<222> (256)..(258)
<223> NNN=ACT OR GTT

<400> 56
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgnnnta ttattgccag acctttggcc agggtacgaa agttgaaatt 300

aaacgtacg 309

<210> 57
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 57
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatgtcta ttatcctga tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 58
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 58
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagactaata atgctcctgt tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 59
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 59
gatatcgtga tgacccagag cccggatagc ctggcggtga gcctgggcga acgtgcgacc 60

attaactgca gaagcagcca gagcgtgctg tatagcagca acaacaaaaa ctatctggcg 120

tggtaccagc agaaaccagg tcagccgccg aaactattaa tttattgggc atccacccgt 180

gaaagcgggg tcccggatcg ttttagcggc tctggatccg gcactgattt taccctgacc 240

atttcgtccc tgcaagctga agacgtggcg gtgtattatt gccagacctt tggccagggt 300

acgaaagttg aaattaaacg tacg 324

<210> 60
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 60
gatatcgtga tgacccagag cccggatagc ctggcggtga gcctgggcga acgtgcgacc 60

attaactgca gaagcagcca gagcgtgctg tatagcagca acaacaaaaa ctatctggcg 120

tggtaccagc agaaaccagg tcagccgccg aaactattaa tttattgggc atccacccgt 180

gaaagcgggg tcccggatcg ttttagcggc tctggatccg gcactgattt taccctgacc 240

atttcgtccc tgcaagctga agacgtggcg gtgtattatt gccagcagta tgattctatt 300

ccttatacct ttggccaggg tacgaaagtt gaaattaaac gtacg 345

<210> 61
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 61
gatatcgcac tgacccagcc agcttcagtg agcggctcac caggtcagag cattaccatc 60

tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120

catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180

agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240

caagcggaag acgaagcgga ttattattgc caggacgtgt ttggcggcgg cacgaagtta 300

accgttcttg gccag 315

<210> 62
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 62
gatatcgcac tgacccagcc agcttcagtg agcggctcac caggtcagag cattaccatc 60

tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120

catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180

agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240

caagcggaag acgaagcgga ttattattgc cagagctatg acatgtataa ttatattgtg 300

tttggcggcg gcacgaagtt aaccgttctt ggccag 336

<210> 63
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 63
gatatcgcac tgacccagcc agcttcagtg agcggctcac caggtcagag cattaccatc 60

tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120

catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180

agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240

caagcggaag acgaagcgga ttattattgc cagtctcatc atttttatga ggtgtttggc 300

ggcggcacga agttaaccgt tcttggccag 330

<210> 64
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 64
gatatcgcac tgacccagcc agcttcagtg agcggctcac caggtcagag cattaccatc 60

tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120

catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180

agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240

caagcggaag acgaagcgga ttattattgc cagagctatg acaataattc tgatgttgtg 300

tttggcggcg gcacgaagtt aaccgttctt ggccag 336

<210> 65
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 65
gatatcgaac tgacccagcc gccttcagtg agcgttgcac caggtcagac cgcgcgtatc 60

tcgtgtagcg gcgatgcgct gggcgataaa tacgcgagct ggtaccagca gaaacccggg 120

caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccaggacgtg tttggcggcg gcacgaagtt aaccgttctt 300

ggccag 306

<210> 66
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 66
gatatcgaac tgacccagcc gccttcagtg agcgttgcac caggtcagac cgcgcgtatc 60

tcgtgtagcg gcgatgcgct gggcgataaa tacgcgagct ggtaccagca gaaacccggg 120

caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccagagctat gactatttta agcttgtgtt tggcggcggc 300

acgaagttaa ccgttcttgg ccag 324

<210> 67
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 67
gatatcgaac tgacccagcc gccttcagtg agcgttgcac caggtcagac cgcgcgtatc 60

tcgtgtagcg gcgatgcgct gggcgataaa tacgcgagct ggtaccagca gaaacccggg 120

caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccagagctat gactattctg ctgattatgt gtttggcggc 300

ggcacgaagt taaccgttct tggccag 327

<210> 68
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 68
gatatcgaac tgacccagcc gccttcagtg agcgttgcac caggtcagac cgcgcgtatc 60

tcgtgtagcg gcgatgcgct gggcgataaa tacgcgagct ggtaccagca gaaacccggg 120

caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccagagctat gactttgatt ttgctgtgtt tggcggcggc 300

acgaagttaa ccgttcttgg ccag 324

<210> 69
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VL domain

<400> 69
gatatcgaac tgacccagcc gccttcagtg agcgttgcac caggtcagac cgcgcgtatc 60

tcgtgtagcg gcgatgcgct gggcgataaa tacgcgagct ggtaccagca gaaacccggg 120

caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccagagctat gacggtcctg atctttgggt gtttggcggc 300

ggcacgaagt taaccgttct tggccag 327

<210> 70

<211> 332
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 70
nnngtgcaat tggttcagtc tggcgcggaa gtgaaaaaac cgggcagcag cgtgaaagtg 60

agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120

cctgggcagg gtctcgagtg gatgggcggc attattccga tttttggcac ggcgaactac 180

gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgattgg 300

ggccaaggca ccctggtgac ggttagctca gc 332

<210> 71
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 71
caggtgcaat tggttcagtc tggcgcggaa gtgaaaaaac cgggcagcag cgtgaaagtg 60

agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120

cctgggcagg gtctcgagtg gatgggcggc attattccga tttttggcac ggcgaactac 180

gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgataat 300

tggtttaagc ctttttctga tgtttggggc caaggcaccc tggtgacggt tagctca 357

<210> 72
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 72
caggtgcaat tggttcagtc tggcgcggaa gtgaaaaaac cgggcagcag cgtgaaagtg 60

agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120

cctgggcagg gtctcgagtg gatgggcggc attattccga tttttggcac ggcgaactac 180

gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgttaat 300

cattggactt atacttttga ttattggggc caaggcaccc tggtgacggt tagctca 357

<210> 73
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 73
caggtgcaat tggttcagtc tggcgcggaa gtgaaaaaac cgggcagcag cgtgaaagtg 60

agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120

cctgggcagg gtctcgagtg gatgggcggc attattccga tttttggcac ggcgaactac 180

gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtggtggt 300

ggttgggttt ctcatggtta ttattatctt tttgatcttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 74
<211> 332
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 74
nnngtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgattgg 300

ggccaaggca ccctggtgac ggttagctca gc 332

<210> 75
<211> 378
<212> DNA

<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 75
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtaatatg 300

gcttatacta attatcagta tgttaatatg cctcattttg attattgggg ccaaggcacc 360

ctggtgacgg ttagctca 378

<210> 76
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 76
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgttctatg 300

aattctacta tgtattggta tcttcgtcgt gttctttttg atcattgggg ccaaggcacc 360

ctggtgacgg ttagctca 378

<210> 77
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 77
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgatttt 300

cttggttatg agtttgatta ttggggccaa ggcaccctgg tgacggttag ctca 354

<210> 78
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 78
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgttattat 300

ggttcttctc tttatcatta tgtttttggt ggttttattg attattgggg ccaaggcacc 360

ctggtgacgg ttagctca 378

<210> 79
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 79
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtggttat 300

tggtatgctt attttactta tattaattat ggttattttg ataattgggg ccaaggcacc 360

ctggtgacgg ttagctca 378

<210> 80
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 80
caggtgcaat tggttcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg 60

agctgcaaag cctccggata tacctttacc agctattata tgcactgggt ccgccaagcc 120

cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtacttgg 300

cagtattctt atttttatta tcttgatggt ggttattatt ttgatatttg gggccaaggc 360

accctggtga cggttagctc a 381

<210> 81
<211> 335
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 81
nnngtgcaat tgaaagaaag cggcccggcc ctggtgaaac cgacccaaac cctgaccctg 60

acctgtacct tttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc 120

cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180

tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg 240

gtgctgacta tgaccaacat ggacccggtg gatacggcca cctattattg cgcgcgtgat 300

tggggccaag gcaccctggt gacggttagc tcagc 335

<210> 82
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 82
caggtgcaat tgaaagaaag cggcccggcc ctggtgaaac cgacccaaac cctgaccctg 60

acctgtacct tttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc 120

cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180

tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg 240

gtgctgacta tgaccaacat ggacccggtg gatacggcca cctattattg cgcgcgttat 300

cattcttggt atgagatggg ttattatggt tctactgttg gttatatgtt tgattattgg 360

ggccaaggca ccctggtgac ggttagctca 390

<210> 83
<211> 341
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<220>
<221> misc_feature
<222> (1)..(3)
<223> NNN=GAA OR CAG

<400> 83
nnngtgcaat tgcaacagtc tggtccgggc ctggtgaaac cgagccaaac cctgagcctg 60

acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120

cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgtag caaatggtat 180

aacgattatg cggtgagcgt gaaaagccgg attaccatca acccggatac ttcgaaaaac 240

cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300

cgtgattggg gccaaggcac cctggtgacg gttagctcag c 341

<210> 84
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> polynucleotide sequence of a VH domain

<400> 84
caggtgcaat tgcaacagtc tggtccgggc ctggtgaaac cgagccaaac cctgagcctg 60

acctgtgcga tttccggaga tagcgtgagc agcaacagcg cggcgtggaa ctggattcgc 120

cagtctcctg ggcgtggcct cgagtggctg ggccgtacct attatcgtag caaatggtat 180

aacgattatg cggtgagcgt gaaaagccgg attaccatca acccggatac ttcgaaaaac 240

cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300

cgttcttatt atcctgattt tgattattgg ggccaaggca ccctggtgac ggttagctca 360

<210> 85
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 85

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln

1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Ser Ala Asp Tyr
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 86
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 86

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser His His Phe Tyr
85 90 95

Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 87
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 87

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asp Phe Ala Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 88
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 88

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val

50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Asp Ser Ile Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr
115

<210> 89
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 89

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Met Ser Asn Tyr Pro
85 90 95

Asp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 90
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> polypeptide sequence of a VL domain

<400> 90

```
Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1               5                  10                  15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Asn
                85                  90                  95

Ser Asp Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105                 110
```

<210> 91
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 91

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Phe Gln Tyr Gly Ser Ile Pro Pro
```

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 92
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 92

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Asn Ala Pro
85 90 95

Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 93
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 93

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Phe Lys Leu Val
85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 94
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 94

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Tyr
85 90 95

Asn Tyr Ile Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

<210> 95
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VL domain

<400> 95

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gly Pro Asp Leu Trp
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105

<210> 96
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 96

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Phe Leu Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 97
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 97

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Gly Ser Ser Leu Tyr His Tyr Val Phe Gly Gly Phe
100 105 110

Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 98
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 98

```
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                  10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Tyr His Ser Trp Tyr Glu Met Gly Tyr Tyr Gly Ser Thr
            100                 105                 110

Val Gly Tyr Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
        115                 120                 125

Ser Ser
    130


<210>  99
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  polypeptide sequence of a VH domain

<400>  99

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Trp Phe Lys Pro Phe Ser Asp Val Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 100
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 100

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Asn His Trp Thr Tyr Thr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 101
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 101

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Trp Tyr Ala Tyr Phe Thr Tyr Ile Asn Tyr Gly Tyr
100 105 110

Phe Asp Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 102
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 102

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Gly Trp Val Ser His Gly Tyr Tyr Tyr Leu Phe Asp
            100                 105                 110

Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 103
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 103

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Thr Trp Gln Tyr Ser Tyr Phe Tyr Tyr Leu Asp Gly Gly Tyr
            100                 105                 110

Tyr Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 104
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 104

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Met Ala Tyr Thr Asn Tyr Gln Tyr Val Asn Met Pro His
100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 105
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> polypeptide sequence of a VH domain

<400> 105

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Met Asn Ser Thr Met Tyr Trp Tyr Leu Arg Arg Val Leu
            100                 105                 110

Phe Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

<210>  106
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  polypeptide sequence of a VH domain

<400>  106

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20                  25                  30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
        35                  40                  45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50                  55                  60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95

Tyr Tyr Cys Ala Arg Ser Tyr Tyr Pro Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```